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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: MEDICAL RESEARCH COUNCIL
- (B) STREET: 20 PARK CRESCENT
- (C) CITY: LONDON
- (E) COUNTRY: UK
- (F) POSTAL CODE (ZIP): W1N 4AL

(ii) TITLE OF INVENTION: GENE

(iii) NUMBER OF SEQUENCES: 16

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 5..604

TGTC ATG TTG CGG GCT TTG AAC CGC CTG GCC GCG CGG CCC GGG GGC CAG  
49

CCC CCA ACC CTG CTC CTT CTG CCC GTG CGC GGC CGC AAG ACC CGC CAC  
97

GAT CCG CCT GCC AAG TCC AAG GTC GGG CGC GTG AAA ATG CCT CCT GCA  
145

GTG GAC CCT GCG GAA TTG TTC GTG TTG ACC GAG CGC TAC CGA CAG TAC  
193

CGG GAG ACG GTG CGC GCT CTC AGG CGA GAG TTC ACA TTG GAG GTG CGA  
241

GGG AAA TTG CAC GAG GCC CGA GCC GGG GTT CTG GCT GAG CGC AAG GCG  
289

CAA GAG GCC ATC AGA GAG CAC CAG GAG CTG ATG GCC TGG AAC CGG GAG  
337

GAG AAC CGG AGA CTG CAG GAA CTA CGG ATA GCT AGG TTG CAG CTC GAA  
385

GCA CAG GCC CAG GAG CTG CGG CAG GCT GAG GTC CAG GCC CAG AGG GCC

433

Ala Gln Ala Gln Glu Leu Arg Gln Ala Glu Val Gln Ala Gln Arg Ala  
130 135 140

CAG GAG GAG CAG GCT TGG GTG CAA CTG AAA GAA CAA GAA GTT CTC AAA  
481

Gln Glu Glu Gln Ala Trp Val Gln Leu Lys Glu Gln Glu Val Leu Lys  
145 150 155

CTG CAG GAG GAG GCC AAA AAC TTC ATC ACT CGG GAG AAC CTG GAG GCA  
529

Leu Gln Glu Glu Ala Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala  
160 165 170 175

CGG ATA GAA GAG GCC TTG GAC TCT CCG AAG AGT TAT AAC TGG GCG GTC  
577

Arg Ile Glu Glu Ala Leu Asp Ser Pro Lys Ser Tyr Asn Trp Ala Val  
180 185 190

ACC AAA GAA GGG CAG GTG GTC AGG AAC TGAGAACAGA GGCCTCTCAG  
624

Thr Lys Glu Gly Gln Val Val Arg Asn  
195 200

GCCCAAATAA GGACAGTGCT TGCCTAGGGA CTGGATATTG GGGTAGAAAT  
TGGTGCATCC 684

CAGGAGGGTG GCACAGCCTT GTCCAGAGCA GCCCCCATTC ATTCTAGATT  
TGGCACCAGG 744

TATAGTACCT GTTCTGACAC CACATACAAA CTCCGGACAG CATTAAACTC  
TGGGAAGTTC 804

CTATCACACA GAAGATCAGA CTGGACTGTC CCCTCTAGAA GCCAAGAGCT  
GTCTCCTGAG 864

TTTCTTGGA TAGTGTGAGC CCAATGTTTC CTGCTTTTAT AAATAAACTA  
TTGGAAAGCA 924

(2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Leu Arg Ala Leu Asn Arg Leu Ala Ala Arg Pro Gly Gly Gln Pro

1 5 10 15

Pro Thr Leu Leu Leu Leu Pro Val Arg Gly Arg Lys Thr Arg His Asp

20 25 30

Pro Pro Ala Lys Ser Lys Val Gly Arg Val Lys Met Pro Pro Ala Val

35 40 45

Asp Pro Ala Glu Leu Phe Val Leu Thr Glu Arg Tyr Arg Gln Tyr Arg

50 55 60

Glu Thr Val Arg Ala Leu Arg Arg Glu Phe Thr Leu Glu Val Arg Gly

65 70 75 80

Lys Leu His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala Gln

85 90 95

Glu Ala Ile Arg Glu His Gln Glu Leu Met Ala Trp Asn Arg Glu Glu

100 105 110

Asn Arg Arg Leu Gln Glu Leu Arg Ile Ala Arg Leu Gln Leu Glu Ala

115 120 125

Gln Ala Gln Glu Leu Arg Gln Ala Glu Val Gln Ala Gln Arg Ala Gln

130 135 140

Glu Glu Gln Ala Trp Val Gln Leu Lys Glu Gln Glu Val Leu Lys Leu

145 150 155 160

Gln Glu Glu Ala Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala Arg

165 170 175

Ile Glu Glu Ala Leu Asp Ser Pro Lys Ser Tyr Asn Trp Ala Val Thr

180 185 190

(2) INFORMATION FOR SEQ ID NO: 3:

(A) LENGTH: 998 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) **HYPOTHETICAL: NO**

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION:1..615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG CTA CGC GCG CTG AGC CGC CTG GGC GCG GGG ACC CCG TGC AGG CCC  
48

Met Leu Arg Ala Leu Ser Arg Leu Gly Ala Gly Thr Pro Cys Arg Pro  
205 210 215

CGG GCC CCT CTG GTG CTG CCA GCG CGC GGC CGC AAG ACC CGC CAC GAC  
96

Arg Ala Pro Leu Val Leu Pro Ala Arg Gly Arg Lys Thr Arg His Asp  
220 225 230

CCG CTG GCC AAA TCC AAG ATC GAG CGA GTG AAC ATG CCG CCC GCG GTG  
144

Pro Leu Ala Lys Ser Lys Ile Glu Arg Val Asn Met Pro Pro Ala Val  
235 240 245

GAC CCT GCG GAG TTC TTC GTG CTG ATG GAG CGT TAC CAG CAC TAC CGC  
192

[illegible]

Val Glu Ala Ala Leu Asp Ser Arg Lys Asn Tyr Asn Trp Ala Ile Thr  
380 385 390

AGA GAG GGG CTG GTG GTC AGG CCA CAA CGC AGG GAC TCC TAGGGGCCCA  
625

Arg Glu Gly Leu Val Val Arg Pro Gln Arg Arg Asp Ser  
395 400 405

GTAAGGACAG TGCCCGCCAG GGACCATGTA TGTATCATGG CGGAAGAGTT  
GGCCCTGACC 685

TGGAATAAAG CAGTTGGTGT TGCTTATGAG GAAGGTTTCAG CCTTATCCAG  
CACAGCCTTC 745

ACGTTTTGCC CTCTGCTGTC ACCACTTGGT CAGAACTTC CAAACGCAGT  
GCCCTGTTCT 805

GCCGGTGTGT AAAGCCTCAG CGCACCAGGA GACCCTAGAG TGGTTTCCAT  
CTCACAGAGA 865

ATCAGACAGG CCACAGCCCC CTCAGGCAGC CAGGTCATCT GAGTATCATT  
AAGAGTAGTG 925

ATGGGAAGAT TACAGTCTGA GGGCCAAACG TGCCTGCTTC CTGTTTTTGT  
AAATAAAGTT 985

TTGTTGGAAC ACA 998

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Leu Arg Ala Leu Ser Arg Leu Gly Ala Gly Thr Pro Cys Arg Pro  
1 5 10 15

Arg Ala Pro Leu Val Leu Pro Ala Arg Gly Arg Lys Thr Arg His Asp  
20 25 30

Pro Leu Ala Lys Ser Lys Ile Glu Arg Val Asn Met Pro Pro Ala Val

35            40            45  
 Asp Pro Ala Glu Phe Phe Val Leu Met Glu Arg Tyr Gln His Tyr Arg  
 50            55            60  
 Gln Thr Val Arg Ala Leu Arg Met Glu Phe Val Ser Glu Val Gln Arg  
 65            70            75            80  
 Lys Val His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala Leu  
 85            90            95  
 Lys Asp Ala Ala Glu His Arg Glu Leu Met Ala Trp Asn Gln Ala Glu  
 100            105            110  
 Asn Arg Arg Leu His Glu Leu Arg Ile Ala Arg Leu Arg Gln Glu Glu  
 115            120            125  
 Arg Glu Gln Glu Gln Arg Gln Ala Leu Glu Gln Ala Arg Lys Ala Glu  
 130            135            140  
 Glu Val Gln Ala Trp Ala Gln Arg Lys Glu Arg Glu Val Leu Gln Leu  
 145            150            155            160  
 Gln Glu Glu Val Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala Arg  
 165            170            175  
 Val Glu Ala Ala Leu Asp Ser Arg Lys Asn Tyr Asn Trp Ala Ile Thr  
 180            185            190  
 Arg Glu Gly Leu Val Val Arg Pro Gln Arg Arg Asp Ser  
 195            200            205

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO



Gln Gln Ala Ile Thr Glu His Arg Glu Leu Met Ala Trp Asn Arg Asp

305 310 315

GAG AAC CGG CGA ATG CAG GAG CTA CGG ATA GCG AGG TTG CAG CTG GAA  
385  
Glu Asn Arg Arg Met Gln Glu Leu Arg Ile Ala Arg Leu Gln Leu Glu  
320 325 330

GCA CAG GCC CAG GAG GTG CAG AAG GCT GAG GCC CAG CGC CAG AGG GCT  
433  
Ala Gln Ala Gln Glu Val Gln Lys Ala Glu Ala Gln Arg Gln Arg Ala  
335 340 345

CAG GAG GAG CAG GCT TGG GTG CAA CTG AAA GAG CAA GAA GTG CTC AAG  
481  
Gln Glu Glu Gln Ala Trp Val Gln Leu Lys Glu Gln Glu Val Leu Lys  
350 355 360

CTG CAG GAG GAG GCA AAA AAC TTC ATC ACT CGG GAG AAC CTG GAG GCA  
529  
Leu Gln Glu Glu Ala Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala  
365 370 375 380

CGG ATA GAA GAA GCG TTG GAC TCT CCG AAG AGT TAC AAC TGG GCC GTC  
577  
Arg Ile Glu Glu Ala Leu Asp Ser Pro Lys Ser Tyr Asn Trp Ala Val  
385 390 395

ACC AAA GAA GGG CAG GTG GTC AGG AAC TGAGCACAGA GACTTCTGGG  
624  
Thr Lys Glu Gly Gln Val Val Arg Asn  
400 405

GGCCCAAATA AGCACAGTGC TTGCCTAGGG TCTGTGTACT GGGATAGGAA  
TTGGTACATC 684

CCAGGAGGAT GGCTCAGCCG TTTCCAGAGC AACCTCAGTC ACTCCAGGCT  
CGGCACTCAC 744

CACCTGACTG GGAAGTCCCA GATGTCCCTG TTCTGGCACC ACAGTCAAAC  
TGAGGGCAGC 804

ATTAAACTCT GGGAAGTTCC TATCGCACAG AGGATCGGAC TGGACTGTGT  
CCCTCTAGAA 864

GCCAAGCTTG TCTTGTAAGT CTCTTGGAGT CCTGTGAGCC AAATGTTTCC  
TGCTTTTATA 924

AATAAAGTAT TGGAGCCCA

943

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Leu Arg Ala Leu Asn Arg Leu Ala Gln Arg Pro Gly Asp Arg Pro  
1 5 10 15

Pro Thr Pro Leu Leu Leu Pro Val Arg Gly Arg Lys Thr Arg His Asp  
20 25 30

Pro Pro Ala Lys Ser Lys Val Gly Arg Val Gln Thr Pro Pro Ala Val  
35 40 45

Asp Pro Ala Glu Phe Phe Val Leu Thr Glu Arg Tyr Gly Gln Tyr Arg  
50 55 60

Glu Thr Val Arg Ala Leu Arg Leu Glu Phe Thr Leu Asp Val Arg Arg  
65                   70                   75                   80

Lys Leu His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala Gln  
85 90 95

Gln Ala Ile Thr Glu His Arg Glu Leu Met Ala Trp Asn Arg Asp Glu  
100 105 110

Asn Arg Arg Met Gln Glu Leu Arg Ile Ala Arg Leu Gln Leu Glu Ala  
115 120 125

Gln Ala Gln Glu Val Gln Lys Ala Glu Ala Gln Arg Gln Arg Ala Gln  
130 135 140

[illegible]

Lys Glu Gly Gln Val Val Arg Asn  
195 200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2852 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Rat 5'OT-EST-xdel

(ix) FEATURE:

- (A) NAME/KEY: exon  
(B) LOCATION:1026..1270

(ix) FEATURE:

- (A) NAME/KEY: exon  
(B) LOCATION:1799..2235

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION:1030..1152

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TGACCTCTGT GGATCTGATA TACATGTAAG TGACAGACCA TCCGAGCTAT  
ATAGTGAGAC 60

CTGTGCAAGG AAGGATGGAG TGCACGTTCC CTGATGTTCA GAGCAACCCT  
GTGTCCTCC 120

AGGTAGGTGA GATGAGAGGA AGAGGGTGGC CTTGGCCTGG GCCTCCTACG  
GGCCTGGAAG 180

TTGGGAGAAG GATGTAAGCA GACTCTGTTT TCTTCTGAGA AATATCAGGT  
ATTGCAGTCA 240

GCCCAGGCTC CTCAGACCCT CCTAAGTGCA GATTCTCTGC AGAATCTGGT  
GTTGACAACA 300

CTAATGAGTA GGATGAGACT TCAGTTCCCT AGCCCTCACC GTCAGCTTCT  
GATTACCAAC 360

AACTCTCCCA GAGGAGAGCC ATCTACCTTT GGGACAGATG CTCTCTGCCC  
TGCACTGCCT 420

CCTGTTTCTC TTCATTGTAG AGGAAGATAG TACTTTAAAA GCTTCATAAA  
TGGTCTCAAG 480

GTGGGAAGAC CCCGGCTCAG GTGAAAGAGG ACAAGCGTCA CCTCACACAG  
GCCACCCAGT 540

AGAAAACAAG TGATCACTGA TACTGAGAAC TCTGGCAATT GCAGAGCTGC  
CCAAGACCAC 600

AACAGGGCAG TGCAATGCAA GGAAAAGGTT TGTTGCTCGA TTGCAAACCT  
AAAGTTTAAA 660

GTGCATCAGG AGAACGCTTA CTCAAAGAGG AAGTGTAAGC CTAACCTAAG  
TAGCTAGAAG 720

CTCAGAATTT CTTGCATCAG CCCTGGAAGG GTACACAGGC CACCGGTGGG  
CCAGAGAACC 780

ACACGCTTTG GGGCGGTGTC CAAGCTTGTG AACAAGTAGG CAAGAGCGCC  
TGGTGTGTA 840

GCTGTCATTG GCGGGCAATA CAGCCCAGCG AACTGTGGTC TCCAAGGTGC  
CCCTCGACCC 900

TCCCACTCTA CCCGAGACTC CAGGGACGCG ATGGGCCAGA CAGCAAGAGC  
TCCGCCTACG 960

GGGGCGGGGA CAGGAGATTC CCGTGATGCT CCTCGACCAC TTCCGGACAG  
GGCGCAGGCG 1020

CTAGCTGTC ATG TTG CGG GCT TTG AAC CGC CTG GCC GCG CGG CCC GGG  
1068

Met Leu Arg Ala Leu Asn Arg Leu Ala Ala Arg Pro Gly  
205 210

GGC CAG CCC CCA ACC CTG CTC CTT CTG CCC GTG CGC GGC CCA CGG CCC  
1116

Gly Gln Pro Pro Thr Leu Leu Leu Leu Pro Val Arg Gly Pro Arg Pro  
215 220 225

CGC TCA TTC TCG GCT CCT TTT TCC TCG CAG GAT AGC TAGGTTGCAG 1162  
Arg Ser Phe Ser Ala Pro Phe Ser Ser Gln Asp Ser  
230 235 240

CTCGAAGCAC AGGCCCAGGA GCTGCGGCAG GCTGAGGTCC AGGCCCAGAG  
GGCCCAGGAG 1222

GAGCAGGCTT GGGTGCAACT GAAAGAACAA GAAGTTCTCA AACTGCAGGT  
GGGCCGAGGT 1282

CGTGAGGAAT GTGGGTATTG GAGATTCCGG TGAGGGAGGC TCTGGGGAGA  
GCAGCACAGG 1342

GTGTCAAGTG ACCAGTCTTC AGGAGGCTTC TCTCTCTGCT CTGCACACAC  
AGAGTGCCTC 1402

CCAGACAATG GTCAATGAAA GGTTACAGGC TAGTATTGCC GTGTGAAACT  
TGAAGGTCAG 1462

GGAAACCATA AATGAGAATG GAGCTGTTTT TATTGTGTAA GGGAGAGTGA  
CAAGGTTGAG 1522

AGAGTCCACC ACCCCGCACC TCCCCCGCC CCCAATCAGG TTGTCACGAT  
TCGATTGTT 1582

1116 1162 1222 1282 1342 1402 1462 1522 1582

AGGGTGCCCC GTTCTCCTG GGAAGGCTC CCGTCAGTG ATTTCTGTAA

CCGGACCCTG 2482

CCCTGACACA GCGTCATTGG ACTACCCAGC AGACAGTAGA CTCCACTCTA  
AACCCGCTTC 2542

TTGCGGTCAG TTGCTGTCCT TCAGTGTGTG TAAGCAGTGG CCAGACAGCA  
CCCTTGGGTG 2602

TCATTTCAAG ACTCTCTCAC CTTGGTCTGC TTTACGTTTG GTTTGATTTG  
GTTTGTTCTG 2662

GTTTTTGAGA CGAGGCCTTT CACTGGAACC TGGCACTCAG TATTTAGACT  
GCCCAGCCAG 2722

CTAGCCTCAG AGAATGCATC TCGGTATGCT TGCCTGGCGC TGGAATTCGG  
TGCACATGGC 2782

TTTGATGTGT ACCGGGGATC AGACACAGAT GTTTCATGAG TGCAGTGCAT  
GCCTGTTAGT 2842

GGTAGAGCTC 2852

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Leu Arg Ala Leu Asn Arg Leu Ala Ala Arg Pro Gly Gly Gln Pro  
1 5 10 15

Pro Thr Leu Leu Leu Leu Pro Val Arg Gly Pro Arg Pro Arg Ser Phe  
20 25 30

Ser Ala Pro Phe Ser Ser Gln Asp Ser  
35 40

(2) INFORMATION FOR SEQ ID NO: 9:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTCACACCAC TCTGTCGAAC

20

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AGGAGGAAGA CAGGTGAAAG

20

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TCATGTTGCG GGCTTTGAAC

20

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: YES

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TCTTTCAGTT GCACCCAAGC

20

## (2) INFORMATION FOR SEQ ID NO: 13:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Synthetic Primer"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GTGATAGGAA CTTCCCAGAG

20

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Synthetic Primer"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GCCTCGTGCA ATTTCCCTCG CACCTCCAAT GTGAACTCTC GC

42

(2) INFORMATION FOR SEQ ID NO: 15:

(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "Synthetic Primer"

(iv) ANTI-SENSE: YES

TCCTGCGAGG AAAAAGGAGC CGAGAATGAG CGGGGCCGTG GG

42

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3264 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Rat 5'OT-EST

(ix) FEATURE:

(A) NAME/KEY: exon w

(B) LOCATION:1026..1241

(ix) FEATURE:

(A) NAME/KEY: exon x  
(B) LOCATION:1332..1478

(ix) FEATURE:  
(A) NAME/KEY: exon y  
(B) LOCATION:1559..1682

(ix) FEATURE:  
(A) NAME/KEY: exon z  
(B) LOCATION:2211..2647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TGACCTCTGT GGATCTGATA TACATGTAAG TGACAGACCA TCCGAGCTAT  
ATAGTGAGAC 60

CTGTGCAAGG AAGGATGGAG TGCACGTTCC CTGATGTTCA GAGCAACCCT  
GTGTCACTCC 120

AGGTAGGTGA GATGAGAGGA AGAGGGTGGC CTTGGCCTGG GCCTCCTACG  
GGCCTGGAAG 180

TTGGGAGAAG GATGTAAGCA GACTCTGTTC TCTTCTGAGA AATATCAGGT  
ATTGCAGTCA 240

GCCCAGGCTC CTCAGACCCT CCTAAGTGCA GATTCTCTGC AGAATCTGGT  
GTTGACAACA 300

CTAATGAGTA GGATGAGACT TCAGTTCCT AGCCCTCACC GTCAGCTTCT  
GATTACCAAC 360

AACTCTCCCA GAGGAGAGCC ATCTACCTTT GGGACAGATG CTCTCTGCCC  
TGCACTGCCT 420

CCTGTTTCTC TTCATTGTAG AGGAAGATAG TACTTTAAAA GCTTCATAAA  
TGGTCTCAAG 480

GTGGGAAGAC CCCGGCTCAG GTGAAAGAGG ACAAGCGTCA CCTCACACAG  
GCCACCCAGT 540

AGAAAACAAG TGATCACTGA TACTGAGAAC TCTGGCAATT GCAGAGCTGC  
CCAAGACCAC 600

AACAGGGCAG TGCAATGCAA GGAAAAGGTT TGTGCTCGA TTGCAAACCT  
AAAGTTTAAA 660

GTGCATCAGG AGAACGCTTA CTCAAAGAGG AAGTGTAAGC CTAAGTTAAG  
TAGCTAGAAG 720

CTCAGAATTT CTTGCATCAG CCCTGGAAGG GTACACAGGC CACCGGTGGG  
CCAGAGAACC 780

ACACGCTTTG GGGCGGTGTC CAAGCTTGTG AACAAGTAGG CAAGAGCGCC  
TGGTGTTGTA 840

GCTGTGATTG GCGGGCAATA CAGCCCAGCG AACTGTGGTC TCCAAGGTGC  
CCCTCGACCC 900

TCCCACTCTA CCCGAGACTC CAGGGACGCG ATGGGCCAGA CAGCAAGAGC  
TCCGCCTACG 960

GGGGCGGGGA CAGGAGATTC CCGTGATGCT CCTCGACCAC TTCCGGACAG  
GGCGCAGGCG 1020

CTAGCTGTCA TGTTGCGGGC TTTGAACCGC CTGGCCGCGC GGCCCGGGGG  
CCAGCCCCCA 1080

ACCCTGCTCC TTCTGCCCCG GCGCGGCCGC AAGACCCGCC ACGATCCGCC  
TGCCAAGTCC 1140

AAGGTCGGGC GCGTGAAAAT GCCTCCTGCA GTGGACCCTG CGGAATTGTT  
CGTGTTGACC 1200

GAGCGCTACC GACAGTACCG GGAGACGGTG CGCGCTCTCA GGTGTGTGTA  
AAGGGCAGGC 1260

GGCCTTCGGC GCCCCCTGGG AAGTGCTGGG GCTGGAGGAT GGGTGCTCAC  
TTGAAGCCCG 1320

TCCTCACCCA GCGGAGAGTT CACATTGGAG GTGCGAGGGA AATTGCACGA  
GGCCCGAGCC 1380

GGGGTTCTGG CTGAGCGCAA GGCGCAAGAG GCCATCAGAG AGCACCAGGA  
GCTGATGGCC 1440

TGGAACCGGG AGGAGAACCG GAGACTGCAG GAACTACGGT GCGAGAGGCG

AGAGTTATAA CTGGGCGGTC ACCAAAGAAG GGCAGGTGGT CAGGAACTGA  
GAACAGAGGC 2340

CTCTCAGGCC CAAATAAGGA CAGTGCTTGC CTAGGGACTG GATATTGGGG  
TAGAAATTGG 2400

TGCATCCCAG GAGGGTGGCA CAGCCTTGTC CAGAGCAGCC CCCATTCATT  
CTAGATTTGG 2460

CACCAGGTAT AGTACCTGTT CTGACACCAC ATACAAACTC CGGACAGCAT  
TAAACTCTGG 2520

GAAGTTCCTA TCACACAGAA GATCAGACTG GACTGTCCCC TCTAGAAGCC  
AAGAGCTGTC 2580

TCCTGAGTTT CTTGGAATAG TGTGAGCCCA ATGTTTCCTG CTTTTATAAA  
TAAACTATTG 2640

GAAAGCAAAG CCTTTTGTTA TGTGGCTTGC TTTTCTTGT TGTAGAATAA  
GTTTATTTGT 2700

CCCAGTTATT TGGGTCTTAA GGTTATTAGC CAAAAGCCAG TTCACCTAAC  
TGAGCCAGGA 2760

GTTAGTTATC TGCTTTGCTC AATCCTGGGC TTTGCTGGGT AGGGTCAGGT  
GTGTCCAAGG 2820

TCCAGAAAGC AAAAAGGGTG CCCC GTTTCT CCTGGGAAGG CTTCCCCGTC  
AGTGATTCT 2880

GTAACCGGAC CCTGCCCTGA CACAGCGTCA TTGGACTACC CAGCAGACAG  
TAGACTCCAC 2940

TCTAAACCCG CTTCTTGCGG TCAGTTGCTG TCCTTCAGTG TGTGTAAGCA  
GTGGCCAGAC 3000

AGCACCTTG GGTGTCATTT CAAGACTCTC TCACCTTGGT CTGCTTTACG  
TTTGGTTTGA 3060

TTTGGTTTGT TCTGGTTTTT GAGACGAGGC CTTTCACTGG AACCTGGCAC  
TCAGTATTTA 3120

GACTGCCCAG CCAGCTAGCC TCAGAGAATG CATCTGCGTA TGCTTGCCTG  
GCGCTGGAAT 3180

TCGGTGCACA TGGCTTTGAT GTGTACCGGG GATCAGACAC AGATGTTTCA

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TGAGTGCAGT 3240

GCATGCCTGT TAGTGGTAGA GCTC

3264

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Cosmid DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GCGGCCGCAT AATACGACTC ACTATAGGGA TCTGGTGGAG GACCTATGGC  
CCGCGAGCTA 60

GAGAAGTGGT TCTCAACCTT CCTAGTGCTG AGACCCTTTA ACACAGTTCC  
TCGTGTTGTG 120

GGGAAACCCC CTCCTGCAAC CATAAAATAA TTTTGTAC TACTTCATAA  
CAAGTGTTGC 180

TACTCTATTG CTATGAATTG TAAAATAAAT GTGTCTTCCA ATGGTCTTAG  
ATGACTCCCG 240

TGAAAGGGTC ATTCTACCCC TAAGAGGTCA TGATCTACAG GTTGAGAACC  
ACTGATCTCC 300

AGTAACCTTC ACTTGAGTCC ATATCCTCCA TGAAGGTATG GAAGTCAATA

AAACTGAGCT 360

TCAAGCCTCA TCAAAATGGG TCCATCCCCT GGTACAGTGT GAGTGGAAGA  
ATACCCACCA 420

TACGGTCACT GGAAGGAGGA TGTCTGAAGG GTCTTAGATT GTGTCAAGGG  
GTCCTGGGTG 480

TCAGGATCTG ACGAAGCAGG CTCGTCATGT TTCATGAAGA CTACAGGTAT  
GTGATAAAAC 540

TGCAAGCTGG AAAAGTACCC ACTGAGCCCG TGTGGCTCTG CTGGGATTTG  
GAGGCATGAG 600

GAGCAGAGGG TCTGGAGGAC AGCAGTCCCA GAAATAATCT ATGACTAAGA  
AGGCTGAACT 660

GGGGTGA CTC TCTGGTGGAA AGAGTTGCCT TTAAAGAAGG AAGACATACC  
AGGCATAGCA 720

ACAACTGCCT TTAGTACTAG CACTCTGAAG GCAGAGGAAG TCCGATTTCT  
CTGAGTTCCA 780

AGCCAGCTTG GTTTACACAG CAAGTTCTAG GCCAACTAGG GTTACATAGT  
GGACTCTCCT 840

CAAACGGGGT TGAGAAAGGA CTCAGCAGTT AGCTCAGTTA ACTCCAGTTC  
TAGGAAATAT 900

GATCCCTTAG TCTGACCTCT TGGCATGTAA GTGGTGCACA TACATATATG  
CACACAAAAT 960

ACATCAATCT GCAAAGGGGG AGGGAGGAAG GGCTGGAGTC TGAAGAAATA  
GTTCACTGGT 1020

TAAGAGAATT CACTGCTCTT CCCAATAGCC AAATTCAGCT CCTAGCATCC  
ATGTCAGATG 1080

GCCCACGAAC ACCTGTAATT CTAGCCCCTA AACTCAGTGC CCCTTCACAA  
GACGGGGACA 1140

CACGTACACA TATACCTAAA AAATTAGGTG GTTTTTTTTT ATTTATAAGG  
TCAAATGCAG 1200

AATATCAAAT GGGTTAGACA GCAGCTCCAA GCTGGCCTCT TCCTCCCAGG  
GCTCTTCTTG 1260

ACTCTTGGCA CCCTCTTTGG GTCCAGAACC CAGACATTAG CCATGACTCA  
GCTGATAAAA 1320

TGCAACCCAT GGCTCATTA TTAGGAAGTC TGTAATTAGC CTGTCTGGTA  
GCCTCCAGAG 1380

AGAACCCTT TCACCTGTCT TCCTCCTCTC ACCCAGGGGA AGAGCTCAGT  
TTTGGCCCTG 1440

AGACAGAAGA AGGGAACGAG ACCATGAGCA ACGGGAAATG AGATGCTGGC  
GCACACACAC 1500

TTTATGTGTG TGAAGTCTCA GAGAGGTCAC CAATAATGAG GCAATGGAAA  
TGAGCTGAGC 1560

TGCCTGAACC TCCAAGTTTC CTCCAAGAAA ACCCCACAGG GGAGATGGGG  
CATGGCCCGAG 1620

GCCAGCTGCC CCAGCCTCTG CTGGCAGAAA GTGAGCCCGC TGCCATTTTA  
ATTTTGTATA 1680

CAGGGTCTCA CTCTACAGCT CTGGGGGCCT AAAACTCACT ATGTAGACTT  
CAAACCTAAC 1740

CAAACCAACA AAAAAACAA AAAAAACCCC TGCACTGACT GGAGAGATGG  
CTCGGTTGAG 1800

AACAATGGCT GCTAGGAGTC AAACCCAGGT CCTGTGGAAG AGCATGCTGG  
TAACTGCTGG 1860

GTCATCGCTG GGTCACCTCTC TTCACACACA CACACACACA CACACACACA  
CACGGCAATG 1920

AACTCTTCAG TGTCTTGATT TACGGTTTCT TCCGATAAAT CCTCAGGAGG  
GCAGTCAAGT 1980

GGCTCATTTG GCAAATGCTT GCCTGAGACC TGAGTTTGGT TCCCAGAACC  
CATGGAGGCA 2040

GAAGGAAAGG GCTCCACAAA GCTCTCTTCT GAACTCCATA TGTGCACACA

GCACACATTC ATAATAGTGA TGAATGAAAA TGAAGACAGA TAAAAAAAAC  
CAATTTCTGTG 2160

AAACTGTTAG CACGTTCAAGT CAATGGCTTT GGGGGTAACC TGTTTCAGAG  
CCATGGTACT 2220

CAGTCACTAG GCTCATACTG GTCAGACGCT GAGGTCAGCA ATGGAGAGCT  
GCTACACCTA 2280

AAGGTAGCAG AGGTCATTG GCTCTGACTC AGAATATTCC AGCTCTCCAC  
ATTCACAGAA 2340

GTTCTACTTG GTCGTAGAAA AAAGCTGAGC CTTTTTTTTT TTTTGGAAC  
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GTCTCATCCT 36180

ACTCATTAGT GTTGTCAACA CCAGATTCTG CAGAGAATCT GCACTTAGGA  
GGGTCTGAGG 36240

AGCCTGGGCT GACTGCAATA CCTGATATTT CTCAGAAGAG AACAGAGTCT  
GCTTACATCC 36300

TTCTCCCAAC TTCCAGGCCC GTAGGAGGCC CAGCCAGCAC CCTCTTCCTC  
TCATCTCACC 36360

CTACCCTGGA GTGACACAGG GTTGCTCTGA ACATCAGGGA ACGTGGCACT  
CCCATCCTTT 36420

CTTGCAACAG GTCTCACTAT ATAGCTCCGG ATGGTCTGTC ACTTACAATG  
TATATCAGAC 36480

TCACAAGAGG TCCATCTGCC ATTGCCTCCT AAATGCTGGG GTTAAAGGCA  
CATACCACCA 36540

CACCTGTCCT AAACCTTTCT TCTTCGGGGT CATCCTAGAT AACCAGTATC  
TCATTCAGA 36600

TAACTTCAGT GTCTGGGCAA AGAGAATATT TCTATGGTGT GGGTCATTCC  
TAGAGGCTTC 36660

CTAACCTTGC TGGCTCTGAC GTTCTCTCGG CTGGTCAGGT CTAATCATCC  
TTCTTTCAGA 36720

GGGTTTCATA AGTTGTAAGA GATTAGGCC TACGGTGGAT GAAAGATGTG  
GAGTCATTTT 36780

GAGTAGCTAA TGCTACAGAA CTAGAAGGCA GGTTCTCTGC CCCCTTCTCT  
GACCTGTTGG 36840

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TAGAATTGTC 36900

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CAGACAGAGT 36960

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TGACTTCAGG 37020

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TCAGGGTCTT 37140

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AGCAATATCC 37200

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ACAGTGATCT 37260

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CTATGAGCAA 37320

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TTAGATCTTC 37380

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TCAGTAGTGA 37440

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TGTGTGCATA 37560

TGGTGCCTAA GTAAAAAAT AATCTTTTAA AAGCAGATT TAAAAAAT  
TTCAACGATT 37620

TTTTTTAAT GTTCATTGGT GTTTTGCCTG CATGTATATC TGTGTGAGGG  
TGTCAGGTTT 37680

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TTGAACCCAG 37740

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TTAGTGTAGA 38640

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CAGAAACTAG 44400

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TGTCTTTCC 44460

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GGGTGGGTGG 44520

CTGGGATGAC CACTTGTAT AGAAAAGAGG AAAAGGAACT GGGAGTTGCG  
GCCGCC 44576

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "Synthetic Primer"

(iv) ANTI-SENSE: NO

GGACAGCCCG AAGGACTACA GGT

23

(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "Synthetic Primer"

(iv) ANTI-SENSE: NO

CGAAGAACTC CGCAGGGTCC

20

(A) LENGTH: 18 base pairs

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AAGACCCGCC ACGACCCG

18

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "Synthetic Primer"

(iii) **HYPOTHETICAL: NO**

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GAATCAGCAC CCTCTCCGCC

20

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Synthetic Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TGCGGAGTTC TTCGTGCTGA TGGAG

25

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Synthetic Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GGTGCTCGGC GCGTCCTTC

20

(2) INFORMATION FOR SEQ ID NO: 24:

25 20 15 10 5 0

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GAGTGGCGGA GAGGGTGCTG A

21

## (2) INFORMATION FOR SEQ ID NO: 25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GGCCGAGGCT GAGCGGGG

18

## (2) INFORMATION FOR SEQ ID NO: 26:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CTGAAGGACG CCGCCGAGCA

20

## (2) INFORMATION FOR SEQ ID NO: 27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CTCCAACGCC TGCCGCTGC

19

## (2) INFORMATION FOR SEQ ID NO: 28:

- (A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GCAGGAGGAG CGGGAGCAGG A

21

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TCCAGTGCCC CGCAAGCCG

19